

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 21, 2006, 14:39:05 ; Search time 37.0181 Seconds  
(without alignments)  
938.721 Million cell updates/sec

Title: US-10-539-834-2

Perfect score: 2135

Sequence: 1 MRCPKCLLSALLTLGLK.....LGQASIRLWKLQDPRLQOC 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/8\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCUS\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                           |
|------------|-------|-------------|--------|-------|---------------------------------------|
| 1          | 2131  | 99.8        | 397    | 2     | US-09-459-133-2 Sequence 2, Appli     |
| 2          | 1595  | 74.7        | 389    | 2     | US-09-459-133-13 Sequence 13, Appli   |
| 3          | 558   | 26.1        | 397    | 3     | US-10-019-735-1 Sequence 1, Appli     |
| 4          | 481   | 22.5        | 378    | 3     | US-10-019-735-4 Sequence 4, Appli     |
| 5          | 467   | 21.9        | 378    | 2     | US-09-482-180A-2 Sequence 2, Appli    |
| 6          | 464.5 | 21.8        | 372    | 3     | US-10-019-735-3 Sequence 3, Appli     |
| 7          | 459.5 | 21.5        | 372    | 3     | US-10-019-735-2 Sequence 2, Appli     |
| 8          | 344.5 | 16.1        | 422    | 2     | US-09-831-630-10 Sequence 10, Appli   |
| 9          | 379.5 | 17.8        | 378    | 2     | US-10-104-047-2503 Sequence 2503, Ap  |
| 10         | 337   | 15.8        | 326    | 1     | US-09-055-097-6 Sequence 6, Appli     |
| 11         | 337   | 15.8        | 326    | 2     | US-09-373-902-6 Sequence 6, Appli     |
| 12         | 337   | 15.8        | 326    | 2     | US-09-831-630-11 Sequence 11, Appli   |
| 13         | 322.5 | 15.1        | 378    | 1     | US-09-055-097-1 Sequence 1, Appli     |
| 14         | 322.5 | 15.1        | 378    | 2     | US-09-373-902-1 Sequence 1, Appli     |
| 15         | 320.5 | 15.0        | 393    | 2     | US-09-949-016-11567 Sequence 11567, A |
| 16         | 320.5 | 15.0        | 378    | 2     | US-09-831-630-13 Sequence 13, Appli   |
| 17         | 314   | 14.7        | 310    | 2     | US-09-831-630-9 Sequence 9, Appli     |
| 18         | 260   | 12.2        | 331    | 2     | US-09-831-630-12 Sequence 12, Appli   |
| 19         | 260   | 12.2        | 331    | 2     | US-09-991-181-209 Sequence 209, App   |
| 20         | 260   | 12.2        | 331    | 2     | US-09-990-444-209 Sequence 209, App   |
| 21         | 260   | 12.2        | 331    | 2     | US-09-997-333-209 Sequence 209, App   |
| 22         | 260   | 12.2        | 331    | 2     | US-09-992-598-209 Sequence 209, App   |
| 23         | 260   | 12.2        | 331    | 2     | US-09-988-735-209 Sequence 209, App   |
| 24         | 260   | 12.2        | 331    | 3     | US-09-989-726-209 Sequence 209, App   |
| 25         | 260   | 12.2        | 331    | 3     | US-09-997-514-209 Sequence 209, App   |
| 26         | 260   | 12.2        | 331    | 3     | US-09-989-728-209 Sequence 209, App   |

|    |       |      |      |   |  |
|----|-------|------|------|---|--|
| 27 | 260   | 12.2 | 331  | 3 | US-09-997-349-209 Sequence 209, App    |
| 28 | 260   | 12.2 | 331  | 3 | US-09-997-653-209 Sequence 209, App    |
| 29 | 260   | 12.2 | 331  | 3 | US-09-989-293A-209 Sequence 209, App   |
| 30 | 258.5 | 12.1 | 325  | 1 | US-09-055-097-5 Sequence 5, Appli      |
| 31 | 258.5 | 12.1 | 325  | 2 | US-09-373-902-5 Sequence 5, Appli      |
| 32 | 166   | 7.8  | 161  | 2 | US-09-270-767-32073 Sequence 32073, A  |
| 33 | 166   | 7.8  | 161  | 2 | US-09-270-767-47290 Sequence 47290, A  |
| 34 | 121.5 | 5.7  | 472  | 2 | US-09-270-767-45443 Sequence 45443, A  |
| 35 | 116.5 | 5.5  | 413  | 2 | US-10-104-047-2399 Sequence 2399, Ap   |
| 36 | 113.5 | 5.3  | 4472 | 1 | US-08-804-227C-2 Sequence 2, Appli     |
| 37 | 112.5 | 5.3  | 872  | 1 | US-08-491-357-3 Sequence 3, Appli      |
| 38 | 112.5 | 5.3  | 872  | 2 | US-08-968-633-3 Sequence 3, Appli      |
| 39 | 112.5 | 5.3  | 872  | 2 | US-09-196-466-3 Sequence 3, Appli      |
| 40 | 112.5 | 5.3  | 872  | 2 | US-09-669-459A-3 Sequence 3, Appli     |
| 41 | 112.5 | 5.3  | 872  | 5 | PCT-US96-10823-3 Sequence 3, Appli     |
| 42 | 112.5 | 5.3  | 3724 | 1 | US-08-804-227C-10 Sequence 10, Appli   |
| 43 | 112.5 | 5.3  | 3724 | 1 | US-08-804-198-4 Sequence 4, Appli      |
| 44 | 111.5 | 5.2  | 1053 | 2 | US-09-902-540-12126 Sequence 12126, A  |
| 45 | 110.5 | 5.2  | 636  | 2 | US-09-252-991A-21770 Sequence 21770, A |

## ALIGNMENTS

RESULT 1  
US-09-459-133-2  
; Sequence 2, Application US/09459133  
; Patent No. 6416988  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Yamamoto, Gayle  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS  
; FILE REFERENCE: 98-77  
; CURRENT APPLICATION NUMBER: US/09/459.133  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/111,697  
; FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (137)...(137)  
; OTHER INFORMATION: Xaa is Gly or Ser  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(397)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-459-133-2

|                       |                 |  |           |             |
|-----------------------|-----------------|--|-----------|-------------|
| Query Match           | 99.8%           | Score 2131;  | DB 2;     | Length 397; |
| Best Local Similarity | 99.7%           | Pred. No. 1.4e-192;  |           |             |
| Matches 396;          | Conservative 0; | Mismatches 1;  | Indels 0; | Gaps 0;     |
| Qy                    | 1               | MRCPKCLLSALLTLGLKVIWTSERLSKAYPSRGTTPPTPANPPTLPANLST        | 60        |             |
| Db                    | 1               | MRCPKCLLSALLTLGLKVIWTSERLSKAYPSRGTTPPTPANPPTLPANLST        | 60        |             |
| Qy                    | 61              | RLGQTIPLPAYWNOQWRGLSGSLPGSTGTGGCOAGAAAATIPDPASYPKDLRRLL    | 120       |             |
| Db                    | 61              | RLGQTIPLPAYWNOQWRGLSGSLPGSTGTGGCOAGAAAATIPDPASYPKDLRRLL    | 120       |             |
| Qy                    | 121             | SAACRSFQMLPGGGGVSSCSDTDPYLLLVKSEPRFAERQAVRETWGSFAPGIRL     | 180       |             |
| Db                    | 121             | SAACRSFQMLPGGGGVSSCSDTDPYLLLVKSEPRFAERQAVRETWGSFAPGIRL     | 180       |             |
| Qy                    | 181             | LFLGLSGVGEAGPDLDSLVAWESRRYDLDLWDFDVPFNTLKDLLLLLAWLGRHCPVTS | 240       |             |
| Db                    | 181             | LFLGLSGVGEAGPDLDSLVAWESRRYDLDLWDFDVPFNTLKDLLLLLAWLGRHCPVTS | 240       |             |

Db 181 LFLGSPVCEAGPDLDSLVAVESRRYSDDLWDFLDPVFNQTLKDLLLAWLGRHCPTVS 240  
 QY 241 FVLRQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRKPFGPPYVPESFFEGG 300  
 Db 241 FVLRQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRKPFGPPYVPESFFEGG 300  
 QY 301 YPAYASGGGVYAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 360  
 Db 301 YPAYASGGGVYAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 360  
 QY 361 DRTADHCAFRNLLVRLPLGPOASIRLWKOLQDPRLQC 397  
 Db 361 DRTADHCAFRNLLVRLPLGPOASIRLWKOLQDPRLQC 397

## RESULT 2

US-09-459-133-13  
 ; Sequence 13, Application US/09459133  
 ; Patent No. 6416988  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Darrell C.  
 ; APPLICANT: Yamamoto, Gayle  
 ; APPLICANT: Jaspers, Stephen R.  
 ; APPLICANT: Gao, Zeren  
 ; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS  
 ; FILE REFERENCE: 98-77  
 ; CURRENT APPLICATION NUMBER: US/09/459,133  
 ; CURRENT FILING DATE: 1999-12-10  
 ; PRIOR APPLICATION NUMBER: 60/111,697  
 ; PRIOR FILING DATE: 1998-12-10  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 13  
 ; LENGTH: 389  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-459-133-13

Query Match 74.7%; Score 1595; DB 2; Length 389;  
 Best Local Similarity 76.1%; Pred. No. 5,2e-142;  
 Matches 302; Conservative 22; Mismatches 65; Indels 8; Gaps 2;  
 QY 1 MRCPCCLLCISALLTLGLKVYIEWTSESLKAYSPRGTPPTPTANDEPTLPANLST 60  
 Db 1 MRCRKQCLLSALLTLGLKVYIEWTSESLKKA--EPRGALPSPTPNNAEPTLPNLSA 58  
 QY 61 RLQOTIPLPAYWQOQWRLGSLPSGSDSTETGTCQAWGAAATEIPDFASYPKDLRRFL 120  
 Db 59 RLQOTGLSSAYWQOQWRLGSLPSGSDSTETGTCQAWGAAATEIPDFASYPKDLRRFL 112  
 QY 121 SAACRSFPQWLPGGGSGVSSCSDTDVYLLAVKSEPGFAERQAVRETGWSPAGIRL 180  
 Db 113 SAACRSFPLWLPAGEGSPVASCSDKDVYLLAVKSEPGHFAARQAVRETGWSPVAGTRL 172  
 QY 181 LFLGSPVCEAGPDLDSLVAVESRRYSDDLWDFLDPVFNQTLKDLLLAWLGRHCPTVS 240  
 Db 173 LFLGSPVCEAGPDLDSLVAVESRRYSDDLWDFLDPVFNQTLKDLLLAWLGRHCPTVS 232  
 QY 241 FVLRQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRKPFGPPYVPESFFEGG 300  
 Db 233 FVLQVQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRKPFGPPYVPESFFEGG 292  
 QY 301 YPAYASGGGVYAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 360  
 Db 293 YPAYASGGGVYAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 352  
 QY 361 DRTADHCAFRNLLVRLPLGPOASIRLWKOLQDPRLQC 397  
 Db 353 EXTRDPCAVRGILLVHPVSPQDTINLWRHLWPELOC 389

## RESULT 3

US-10-019-735-1

; Sequence 1, Application US/10019735  
 ; Patent No. 7005279  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
 ; TITLE OF INVENTION: No. 7005279e1 Polypeptides  
 ; FILE REFERENCE: 11216W01  
 ; CURRENT APPLICATION NUMBER: US/10/019,735  
 ; CURRENT FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: JP 99/183437  
 ; PRIOR FILING DATE: 1999-06-29  
 ; PRIOR APPLICATION NUMBER: JP 2000/74757  
 ; PRIOR FILING DATE: 2000-03-16  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 397  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-019-735-1

Query Match 26.1%; Score 558; DB 3; Length 397;  
 Best Local Similarity 34.5%; Pred. No. 3.9e-44;  
 Matches 121; Conservative 69; Mismatches 131; Indels 30; Gaps 8;  
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 Db 55 PFAYWQOQWRLG-----SLPSGSDSTETGG-----COAWGAAATEIPDFASYP 113  
 QY 113 KDLRRFLLSAACSFPQWLPGGGSGVSSCSDTDVYLLAVKSEPGFAERQAVRETGW 172  
 Db 114 DRFKDFLLYLRCHRYSLII-----DQDKCAKK--PFLLLAIAKSLTPHFARRQAIRSWG 166  
 QY 173 SPAPG---IRLLPLLG-SPVGEAGPDLDSLVAVESRRYSDDLWDFLDPVFNQTLKDLL 227  
 Db 167 QESNAGNQTVRVFLGQTPPEONHPDLSMDLKFSEKHQDILWNYRFFNLSLKEVL 226  
 QY 228 LLAWLGRHCPTVSFVLRQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRKP 287  
 Db 227 FLRWSTSCPDTEFVKGDDDFVNTTHILNLSLTKAKOLFIDGVHINAGPHRDKK 286  
 QY 288 GPYVPESFFEGGYPAYASGGGVYAGRLAPKLLRAARVAPFPEDVYTGICIRALGLV 347  
 Db 287 LKYIPEVYVYSGLYPPYAGGGGFLYSGHIALRLYHITDQVHLYPIDDVYTGICIRALGLV 346  
 QY 348 POAHGFLTAWPADRTADH-CAFRNLLVRLPLGPOASIRLWKOLQDPRLQC 397  
 Db 347 PEKHGFRFTDIEKKNNICSYVDLMLVHSRKPQEMIDIWSQSAHLKC 397

## RESULT 4

US-10-019-735-4  
 ; Sequence 4, Application US/10019735  
 ; Patent No. 7005279  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
 ; TITLE OF INVENTION: No. 7005279e1 Polypeptides  
 ; FILE REFERENCE: 11216W01  
 ; CURRENT APPLICATION NUMBER: US/10/019,735  
 ; CURRENT FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: JP 99/183437  
 ; PRIOR FILING DATE: 1999-06-29  
 ; PRIOR APPLICATION NUMBER: JP 2000/74757  
 ; PRIOR FILING DATE: 2000-03-16  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 378  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-019-735-4

Query Match 22.5%; Score 481; DB 3; Length 378;  
 Best Local Similarity 33.1%; Pred. No. 6.7e-37;

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2006, 14:39:05 ; Search time 34.687 Seconds  
(without alignments)  
938.721 Million cell updates/sec

Title: US-10-539-834-16

Perfect score: 1999

Sequence: 1 TSESLSKAYSPRGTPPSP.....LGPQASIRLWQLQDPRLOC 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/iaa/5 COMB.pap:\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/iaa/6 COMB.pap:\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/iaa/7 COMB.pap:\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/iaa/H COMB.pap:\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/iaa/PCTUS COMB.pap:\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/iaa/RE COMB.pap:\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                           |
|------------|-------|-------------|--------|-------|---------------------------------------|
| 1          | 1395  | 99.8        | 397    | 2     | US-09-459-133-2 Sequence 2, Appli     |
| 2          | 1474  | 73.7        | 389    | 2     | US-09-459-133-13 Sequence 13, Appli   |
| 3          | 558   | 27.9        | 397    | 3     | US-10-019-735-1 Sequence 1, Appli     |
| 4          | 474.5 | 23.7        | 378    | 3     | US-10-019-735-4 Sequence 4, Appli     |
| 5          | 464.5 | 23.2        | 372    | 3     | US-10-019-735-3 Sequence 3, Appli     |
| 6          | 460.5 | 23.0        | 378    | 2     | US-09-482-180A-2 Sequence 2, Appli    |
| 7          | 459.5 | 23.0        | 372    | 3     | US-10-019-735-2 Sequence 2, Appli     |
| 8          | 375.5 | 19.0        | 378    | 2     | US-10-104-047-2503 Sequence 2503, Ap  |
| 9          | 344.5 | 17.2        | 422    | 2     | US-09-831-630-10 Sequence 10, Appli   |
| 10         | 337   | 16.9        | 326    | 1     | US-09-055-097-6 Sequence 6, Appli     |
| 11         | 337   | 16.9        | 326    | 2     | US-09-373-902-6 Sequence 6, Appli     |
| 12         | 337   | 16.9        | 326    | 2     | US-09-831-630-11 Sequence 11, Appli   |
| 13         | 322.5 | 16.1        | 378    | 1     | US-09-055-097-1 Sequence 1, Appli     |
| 14         | 322.5 | 16.1        | 378    | 2     | US-09-373-902-1 Sequence 1, Appli     |
| 15         | 322.5 | 16.0        | 393    | 2     | US-09-949-016-11567 Sequence 11567, A |
| 16         | 320.5 | 16.0        | 378    | 2     | US-09-831-630-13 Sequence 13, Appli   |
| 17         | 314   | 15.7        | 310    | 2     | US-09-831-630-9 Sequence 9, Appli     |
| 18         | 260   | 13.0        | 331    | 2     | US-09-831-630-12 Sequence 12, Appli   |
| 19         | 260   | 13.0        | 331    | 2     | US-09-991-181-209 Sequence 209, App   |
| 20         | 260   | 13.0        | 331    | 2     | US-09-990-444-209 Sequence 209, App   |
| 21         | 260   | 13.0        | 331    | 2     | US-09-997-333-209 Sequence 209, App   |
| 22         | 260   | 13.0        | 331    | 2     | US-09-992-598-209 Sequence 209, App   |
| 23         | 260   | 13.0        | 331    | 2     | US-09-989-735-209 Sequence 209, App   |
| 24         | 260   | 13.0        | 331    | 3     | US-09-989-726-209 Sequence 209, App   |
| 25         | 260   | 13.0        | 331    | 3     | US-09-997-514-209 Sequence 209, App   |
| 26         | 260   | 13.0        | 331    | 3     | US-09-989-728-209 Sequence 209, App   |

|    |       |      |      |   |  |
|----|-------|------|------|---|--|
| 27 | 260   | 13.0 | 331  | 3 | US-09-997-349-209 Sequence 209, App    |
| 28 | 260   | 13.0 | 331  | 3 | US-09-997-653-209 Sequence 209, App    |
| 29 | 260   | 13.0 | 331  | 3 | US-09-989-293A-209 Sequence 209, App   |
| 30 | 258.5 | 12.9 | 325  | 1 | US-09-055-097-5 Sequence 5, Appli      |
| 31 | 258.5 | 12.9 | 325  | 2 | US-09-373-902-5 Sequence 5, Appli      |
| 32 | 166   | 8.3  | 161  | 2 | US-09-270-767-32073 Sequence 32073, A  |
| 33 | 166   | 8.3  | 161  | 2 | US-09-270-767-47290 Sequence 47290, A  |
| 34 | 121.5 | 6.1  | 472  | 2 | US-09-270-767-47290 Sequence 47290, A  |
| 35 | 112.5 | 5.6  | 872  | 1 | US-08-491-357-3 Sequence 3, Appli      |
| 36 | 112.5 | 5.6  | 872  | 2 | US-08-968-633-3 Sequence 3, Appli      |
| 37 | 112.5 | 5.6  | 872  | 2 | US-09-196-466-3 Sequence 3, Appli      |
| 38 | 112.5 | 5.6  | 872  | 2 | US-09-669-459A-3 Sequence 3, Appli     |
| 39 | 112.5 | 5.6  | 872  | 5 | PCT-US96-10823-3 Sequence 3, Appli     |
| 40 | 112.5 | 5.6  | 3724 | 1 | US-08-804-227C-10 Sequence 10, Appli   |
| 41 | 112.5 | 5.6  | 3724 | 1 | US-08-804-198-4 Sequence 4, Appli      |
| 42 | 112   | 5.6  | 4472 | 1 | US-08-804-227C-2 Sequence 2, Appli     |
| 43 | 111.5 | 5.6  | 1053 | 2 | US-09-902-540-12126 Sequence 12126, A  |
| 44 | 110.5 | 5.5  | 636  | 2 | US-09-252-991A-21770 Sequence 21770, A |
| 45 | 109   | 5.5  | 794  | 2 | US-09-252-991A-28569 Sequence 28569, A |

## ALIGNMENTS

RESULT 1  
US-09-459-133-2  
; Sequence 2, Application US/09459133  
; Patent No. 6416988  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Yamamoto, Gayle  
; APPLICANT: Jaepers, Stephen R.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS  
; FILE REFERENCE: 98-77  
; CURRENT APPLICATION NUMBER: US/09/459,133  
; CURRENT FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/111,697  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (137)...(137)  
; OTHER INFORMATION: Xaa is Gly or Ser  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(397)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-459-133-2

Query Match 99.8%; Score 1995; DB 2; Length 397;  
Best Local Similarity 99.7%; Pred. No. 9.9e-183;  
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TSESLSKAYSPRGTPPSPANPEPTLPANLSTRGLGQTIPLPAYNQOOWRLGSLPS 60  
Db 26 TSESLSKAYSPRGTPPSPANPEPTLPANLSTRGLGQTIPLPAYNQOOWRLGSLPS 85  
Qy 61 GDSLETGCGQAWGAAATEIPDFASYPKDLRRLLSAAACRSFPQWLPGGGSGQVSSCSDT 120  
Db 86 GDSLETGCGQAWGAAATEIPDFASYPKDLRRLLSAAACRSFPQWLPGGGSGQVSSCSDT 145  
Qy 121 DVPYLLAVKSEPGRFAERQAVRETWGSPPAGIRLLFLGSPVGEAGDPDLSLWAVESRR 180  
Db 146 DVPYLLAVKSEPGRFAERQAVRETWGSPPAGIRLLFLGSPVGEAGDPDLSLWAVESRR 205  
Qy 181 YSDILLWDFVDPNOKDKLLLLAWLGRHCPVSVFLRAODDAFVHTPALLAHRLALPP 240

Db 206 YSDLLWDLVDFVFNQTLKDLLLAWLGRHCHCTVSFVLRQDDAFVHTPALLAHLRALPP 265  
 QY 241 ASARSLYLGEVFTQAMPLKPGPFVPSRFFEGGYVAYASGGVVIAGRLAPWLLRAAA 300  
 Db 266 ASARSLYLGEVFTQAMPLKPGPFVPSRFFEGGYVAYASGGVVIAGRLAPWLLRAAA 325  
 QY 301 RVAPPPFDVYTGICIRALGLVQAHGFLTAMPADRTADHCAFRNLLVRLPLGQASIR 360  
 Db 326 RVAPPPFDVYTGICIRALGLVQAHGFLTAMPADRTADHCAFRNLLVRLPLGQASIR 385  
 QY 361 LWKQLQDRLOC 372  
 Db 386 LWKQLQDRLOC 397

RESULT 2  
 US-09-459-133-13  
 ; Sequence 13, Application US/09459133  
 ; Patent No. 641698  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Darrell C.  
 ; APPLICANT: Yamamoto, Gayle  
 ; APPLICANT: Jaspers, Stephen R.  
 ; APPLICANT: Gao, Zeren  
 ; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS  
 ; FILE REFERENCE: 98-77  
 ; CURRENT APPLICATION NUMBER: US/09/459,133  
 ; CURRENT FILING DATE: 1999-12-10  
 ; PRIOR APPLICATION NUMBER: 60/111,697  
 ; PRIOR FILING DATE: 1998-12-10  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 13  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-459-133-13

Query Match 73.7%; Score 1474; DB 2; Length 389;  
 Best Local Similarity 75.0%; Pred. No. 8.5e-133;  
 Matches 279; Conservative 22; Mismatches 63; Indels 8; Gaps 2;  
 QY 1 TSERLSKAYPSRGRTPPPTPANPEPTLPANLSTRLGOTIPLPAYWQOQWRLGSLPS 60  
 Db 26 TSERLWKKK--EPGALPSPTPPNABPTLPNLNLSRLGOTGPLSSAYWQOQWRLGSLPS 83  
 QY 61 GDSLETGGCOAGAAATEIPDPASYPKOLRLRLLSAACRSFQWLPGGGGSOVSSCSDT 120  
 Db 84 TD-----COTGTVAASEILDFILYPOELRRLFLLSAACRSFPLWLPAGEGSPVASCSDK 137  
 QY 121 DVPYLLAVKSPGFAERQAVRETGWSPAPGIRLLFLGSPVGEAGPDLDSIYAVESRR 180  
 Db 138 DVPYLLAVKSPGFAERQAVRETGWSPVAGTRLLFLGSPVGEAGPDLDSIYAVESRR 197  
 QY 181 YSDLLWDLVDFVFNQTLKDLLLAWLGRHCHCTVSFVLRQDDAFVHTPALLAHLRALPP 240  
 Db 198 YGDLWDLVDFVFNQTLKDLLLAWLGRHCHCTVSFVLRQDDAFVHTPALLAHLRALPP 257  
 QY 241 ASARSLYLGEVFTQAMPLKPGPFVPSRFFEGGYVAYASGGVVIAGRLAPWLLRAAA 300  
 Db 258 TWARSYLGEIETQAKPLKPGPFVPSRFFEGGYVAYASGGVVIAGRLAPWLLRAAA 317  
 QY 301 RVAPPPFDVYTGICIRALGLVQAHGFLTAMPADRTADHCAFRNLLVRLPLGQASIR 360  
 Db 318 RVAPPPFDVYTGICIRALGLVQAHGFLTAMPADRTADHCAFRNLLVRLPLGQASIR 377  
 QY 361 LWKQLQDRLOC 372  
 Db 378 LWRHLWVPELOC 389

RESULT 3  
 US-10-019-735-1

; Sequence 1, Application US/10019735  
 ; Patent No. 7005279  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
 ; TITLE OF INVENTION: No. 7005279e1 Polypeptides  
 ; FILE REFERENCE: 11216W01  
 ; CURRENT APPLICATION NUMBER: US/10/019,735  
 ; CURRENT FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: JP 99/183437  
 ; PRIOR FILING DATE: 1999-06-29  
 ; PRIOR APPLICATION NUMBER: JP 2000/74757  
 ; PRIOR FILING DATE: 2000-03-16  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 397  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-019-735-1

Query Match 27.9%; Score 558; DB 3; Length 397;  
 Best Local Similarity 34.5%; Pred. No. 5.7e-45;  
 Matches 121; Conservative 69; Mismatches 131; Indels 30; Gaps 8;  
 QY 44 PPAVWQOQWRLG-----SLPSGDSSTGCG-----COAGAAATEIPDPASYP 87  
 Db 55 PEAYWREOEKLNROYNPILSMLTNTQTEAGRLNLSHLYNCEP-DLRVTSVVTGFNNLP 113  
 QY 88 KDLRRELLAAACRSFPQWLPGGGGSOVSSCSDTDPVYLLAVKSEPCRAERQAVRETGW 147  
 Db 114 DRFKDFLLVRCNYSLLI-----DQDCAKK--PFLLAIKSLTPTFHARQAIRESWG 166  
 QY 148 SPAG-----IRLDFLLG-SPVGEAGPDLDSIYAVESRRYSDLLWDLVDFVFNQTLKDLL 202  
 Db 167 QESNAGNQTWVRFVFLGOTPPEDNHPDLSDMLKFESEKQDILMWNRYDTFFNLSLKEVL 226  
 QY 203 LLAWLGRHCHCTVSFVLRQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLKPG 262  
 Db 227 FURWSTSCPDTEFFVFGDDVFNTHILNLSLSTKAKDKLFTIGDVIHNAHPHRDKK 286  
 QY 263 GPFYVPSFEGGYVAYASGGVVIAGRLAPWLLRAAAARVAPPPFDVYTGICIRALGLV 322  
 Db 287 LKYYIPEVYVSLYPPYAGGGGFVSGHLALRLYHTDOVHLYPDDVYTGICIRALGLV 346  
 QY 323 QOAHGFLTAMPADRTADH-CAFRNLLVRLPLGQASIRLWKLQDRLOC 372  
 Db 347 PEKHGFRFTDEEKNKNICSYVDLMVHSRKQEMIDINWQLOSAHLKC 397

RESULT 4  
 US-10-019-735-4  
 ; Sequence 4, Application US/10019735  
 ; Patent No. 7005279  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
 ; TITLE OF INVENTION: No. 7005279e1 Polypeptides  
 ; FILE REFERENCE: 11216W01  
 ; CURRENT APPLICATION NUMBER: US/10/019,735  
 ; CURRENT FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: JP 99/183437  
 ; PRIOR FILING DATE: 1999-06-29  
 ; PRIOR APPLICATION NUMBER: JP 2000/74757  
 ; PRIOR FILING DATE: 2000-03-16  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 378  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-019-735-4

Query Match 23.7%; Score 474.5; DB 3; Length 378;  
 Best Local Similarity 39.3%; Pred. No. 5.4e-37;

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 21, 2006, 14:39:05 ; Search time 26.295 Seconds  
(without alignments)  
938.721 Million cell updates/sec

Title: US-10-539-834-17

Perfect score: 1508

Sequence: 1 RRFLLSACRSFPQWLPGGG.....LGPOASIRLWKQLQDPRLQC 282

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*
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  - 2: /EMC Celerra\_IDS3/ptodata/2/iaa/6\_COMB.pep.\*
  - 3: /EMC Celerra\_IDS3/ptodata/2/iaa/7\_COMB.pep.\*
  - 4: /EMC Celerra\_IDS3/ptodata/2/iaa/H\_COMB.pep.\*
  - 5: /EMC Celerra\_IDS3/ptodata/2/iaa/PTUS\_COMB.pep.\*
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  - 7: /EMC Celerra\_IDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 1504  | 99.7        | 397    | 2     | US-09-459-133-2     |
| 2          | 1206  | 80.0        | 389    | 2     | US-09-459-133-13    |
| 3          | 526.5 | 34.9        | 397    | 3     | US-10-019-735-1     |
| 4          | 469.5 | 31.1        | 378    | 3     | US-10-019-735-4     |
| 5          | 455.5 | 30.2        | 378    | 2     | US-09-482-180A-2    |
| 6          | 427.5 | 28.3        | 372    | 3     | US-10-019-735-3     |
| 7          | 422.5 | 28.0        | 372    | 3     | US-10-019-735-2     |
| 8          | 379.5 | 25.2        | 378    | 2     | US-10-104-047-2503  |
| 9          | 344.5 | 22.8        | 422    | 2     | US-09-831-630-10    |
| 10         | 337   | 22.3        | 326    | 1     | US-09-055-097-6     |
| 11         | 337   | 22.3        | 326    | 2     | US-09-373-902-6     |
| 12         | 337   | 22.3        | 326    | 2     | US-09-831-630-11    |
| 13         | 322   | 21.4        | 378    | 1     | US-09-055-097-1     |
| 14         | 322   | 21.4        | 378    | 2     | US-09-373-902-1     |
| 15         | 322   | 21.4        | 393    | 2     | US-09-949-016-11567 |
| 16         | 320   | 21.2        | 378    | 2     | US-09-831-630-13    |
| 17         | 314   | 20.8        | 310    | 2     | US-09-831-630-9     |
| 18         | 260   | 17.2        | 331    | 2     | US-09-831-630-12    |
| 19         | 260   | 17.2        | 331    | 2     | US-09-991-181-209   |
| 20         | 260   | 17.2        | 331    | 2     | US-09-990-444-209   |
| 21         | 260   | 17.2        | 331    | 2     | US-09-997-333-209   |
| 22         | 260   | 17.2        | 331    | 2     | US-09-992-598-209   |
| 23         | 260   | 17.2        | 331    | 2     | US-09-989-735-209   |
| 24         | 260   | 17.2        | 331    | 3     | US-09-989-726-209   |
| 25         | 260   | 17.2        | 331    | 3     | US-09-997-514-209   |
| 26         | 260   | 17.2        | 331    | 3     | US-09-989-728-209   |

|    |       |      |      |   |                      |                   |
|----|-------|------|------|---|----------------------|-------------------|
| 27 | 260   | 17.2 | 331  | 3 | US-09-997-349-209    | Sequence 209, App |
| 28 | 260   | 17.2 | 331  | 3 | US-09-997-853-209    | Sequence 209, App |
| 29 | 260   | 17.2 | 331  | 3 | US-09-989-293A-209   | Sequence 209, App |
| 30 | 258.5 | 17.1 | 325  | 1 | US-09-055-097-5      | Sequence 5, Appli |
| 31 | 258.5 | 17.1 | 325  | 2 | US-09-373-902-5      | Sequence 5, Appli |
| 32 | 166   | 11.0 | 161  | 2 | US-09-270-767-32073  | Sequence 32073, A |
| 33 | 166   | 11.0 | 161  | 2 | US-09-270-767-47290  | Sequence 47290, A |
| 34 | 121.5 | 8.1  | 472  | 2 | US-09-270-767-45443  | Sequence 45443, A |
| 35 | 105.5 | 7.0  | 113  | 2 | US-09-270-767-46296  | Sequence 46296, A |
| 36 | 105.5 | 7.0  | 113  | 2 | US-09-270-767-61866  | Sequence 61866, A |
| 37 | 101   | 6.7  | 174  | 2 | US-09-270-767-60949  | Sequence 60949, A |
| 38 | 99    | 6.6  | 648  | 2 | US-09-489-039A-10538 | Sequence 10538, A |
| 39 | 95    | 6.3  | 372  | 1 | US-08-207-904-10     | Sequence 10, Appl |
| 40 | 93.5  | 6.2  | 542  | 2 | US-09-252-991A-26356 | Sequence 26356, A |
| 41 | 93    | 6.2  | 274  | 2 | US-09-252-991A-24164 | Sequence 24164, A |
| 42 | 92.5  | 6.1  | 1911 | 1 | US-08-348-006B-5     | Sequence 5, Appli |
| 43 | 92.5  | 6.1  | 1911 | 1 | US-08-800-825A-5     | Sequence 5, Appli |
| 44 | 92.5  | 6.1  | 1911 | 2 | US-09-158-657-5      | Sequence 5, Appli |
| 45 | 92.5  | 6.1  | 1911 | 5 | PCT-US94-10166-5     | Sequence 5, Appli |

## ALIGNMENTS

RESULT 1  
US-09-459-133-2  
; Sequence 2, Application US/09459133  
; Patent No. 6416988  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Yamamoto, Gayle  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS  
; FILE REFERENCE: 98-77  
; CURRENT APPLICATION NUMBER: US/09/459,133  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (137)...(137)  
; OTHER INFORMATION: Xaa is Gly or Ser  
; FEATURES:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(397)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-459-133-2

Query Match 99.7%; Score 1504; DB 2; Length 397;  
Best Local Similarity 99.6%; Pred. No. 6.2e-149;  
Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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| Qy | 1   | RRFLSACRSFPQWLPGGGGQVSSCSDTDPVYLLAVKSEPGRFABQAVRTWGS       | 60  |
| Db | 116 | RRFLSACRSFPQWLPGGGGQVSSCSDTDPVYLLAVKSEPGRFABQAVRTWGS       | 175 |
| Qy | 61  | PGIRLLFILASPVGEAGPDLDSLVAWESRRYSDDLMLDFLDVFPNQTLLKLLALLGRH | 120 |
| Db | 176 | PGIRLLFILASPVGEAGPDLDSLVAWESRRYSDDLMLDFLDVFPNQTLLKLLALLGRH | 235 |
| Qy | 121 | CPTVSVFLRAODDAFVHTPALLAHLRALPPASASLYLGEVFTQAMPLKPGGPPVDES  | 180 |
| Db | 236 | CPTVSVFLRAODDAFVHTPALLAHLRALPPASASLYLGEVFTQAMPLKPGGPPVDES  | 295 |
| Qy | 181 | PFEGGYPAYASGGGVYTAGRLAPWLLRAAAAVAPFPFEDVYTGICIRALGVPOAHGFL | 240 |

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Db 296 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 355
QY 241 TAWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 282
Db 356 TAWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 397

RESULT 2
US-09-459-133-13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-019-735-1
Query Match 34.9%; Score 526.5; DB 3; Length 397;
Best Local Similarity 37.8%; Pred. No. 1.6e-46;
Matches 108; Conservative 58; Mismatches 107; Indels 13; Gaps 5;

QY 3 FLLSAACRSFPQWLPGGGGSOVSSCSDTDVPYLLAVKSEPGFAERQAVRTWGSAPG 62
Db 119 FLYLRCRNYSLI-----DQPKCAKK--PELLAIKSLTTHFAARQAIRESWGQESNA 171
QY 63 ----IRLLFLLG-SPVGEAGPDLDSLVAVESRRYSDDLWDFLDVPFNQTLKDLLLAWL 117
Db 172 GNOTVVRVFLGQTPEPDHNPDLSDMLKFESEKHQDILWNYRDFFNLSEVLEFLRVV 231
QY 118 GRHCTVSVFLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGPFYV 177
Db 232 STSCPDTEBFVKGDDDDVFVNTHHILNLYLSLSTKAKDLFIGDVHNAHPHRDKLKYVI 291
QY 178 PSEFEGGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAH 237
Db 292 FEVYSGLYPPYAGGGGFLYSGHLALRLYHTDQVHLYPDIDVYTGMCLOKLGLVPERKH 351
QY 238 GFLTAPADRTADH-CAFRNLLVRLPGQASIRLWKOLQDPRLOC 282
Db 352 GFRTDIEBKNNICSYVDLMLVHSRKPQEMIDISQLOSAHLKC 397

RESULT 4
US-10-019-735-4
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-019-735-1
Query Match 31.1%; Score 469.5; DB 3; Length 378;
Best Local Similarity 39.4%; Pred. No. 1.4e-40;
Matches 115; Conservative 38; Mismatches 114; Indels 25; Gaps 10;

QY 1 RRFLLSAACRSFPQWLPGGGGSOVSSCS-DTDVPYLLAVKSEPGFAERQAVRTWGS- 57
Db 94 RLFTYRHCNFSILL-----EPGGSKDT---FLLAIKSGQHVERRAIRSTGRV 144
QY 58 ---SPAFGIRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDVPFNQTLKDLLL 114
Db 145 GQWARGRLKLVFLLG-VAGSAPP--AQLLAYESREFDILLQWDFTEDEFNLTJLKLHLQ 201
QY 115 AYLGRHCTVSVFLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGP 174
Db 202 RWWAACPCQAHFMKGGDDDFVHVNVLEFLDGWDP--AQDLLVGDVIRQALPNRNTKVK 259
QY 175 FYVPESPFEG-GYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLV 233
Db 260 YFIPPSMYRATHYPPYAGGGYVMSRATVRRLQAIMEDAEFLPIDDVFGVCLRLGLSP 319
QY 234 QAHPGFLT---AWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 282
; LENGTH: 397
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Db 296 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 355
QY 241 TAWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 282
Db 356 TAWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 397

RESULT 2
US-09-459-133-13
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-459-133-13
Query Match 80.0%; Score 1206; DB 2; Length 389;
Best Local Similarity 78.4%; Pred. No. 9.9e-118;
Matches 222; Conservative 18; Mismatches 42; Indels 0; Gaps 0;

QY 1 RRFLLSAACRSFPQWLPGGGGSOVSSCSDTDVPYLLAVKSEPGFAERQAVRTWGS 60
Db 108 RFLLSAACRSFPLMPAGEGSEVASCSDKQVPYLLAVKSEPGFAERQAVRTWGS 167
QY 61 FGIRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDVPFNQTLKDLLLAWLGRH 120
Db 168 AGTRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDVPFNQTLKDLLLAWLGRH 227
QY 121 GPTVSVFLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGPFYV 180
Db 228 CPDVNFVLQVODDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGPFYV 287
QY 181 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 240
Db 288 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 347
QY 241 TAWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 282
Db 348 TAWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 389

RESULT 3
US-10-019-735-1
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-019-735-1
Query Match 31.1%; Score 469.5; DB 3; Length 378;
Best Local Similarity 39.4%; Pred. No. 1.4e-40;
Matches 115; Conservative 38; Mismatches 114; Indels 25; Gaps 10;

QY 1 RRFLLSAACRSFPQWLPGGGGSOVSSCS-DTDVPYLLAVKSEPGFAERQAVRTWGS- 57
Db 94 RLFTYRHCNFSILL-----EPGGSKDT---FLLAIKSGQHVERRAIRSTGRV 144
QY 58 ---SPAFGIRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDVPFNQTLKDLLL 114
Db 145 GQWARGRLKLVFLLG-VAGSAPP--AQLLAYESREFDILLQWDFTEDEFNLTJLKLHLQ 201
QY 115 AYLGRHCTVSVFLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGP 174
Db 202 RWWAACPCQAHFMKGGDDDFVHVNVLEFLDGWDP--AQDLLVGDVIRQALPNRNTKVK 259
QY 175 FYVPESPFEG-GYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLV 233
Db 260 YFIPPSMYRATHYPPYAGGGYVMSRATVRRLQAIMEDAEFLPIDDVFGVCLRLGLSP 319
QY 234 QAHPGFLT---AWPADRTADHCAFRNLLVRLPGQASIRLWKOLQDPRLOC 282
; LENGTH: 397
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